

SEQUENCE LISTING

<110> GONG, Zhiyuan
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 JU, Bensheng
 XU, Yanfei
 -- HE, Jiangyan
 YAN, Tie

<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
 TRANSGENIC ORNAMENTAL FISH

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<170> PatentIn Ver. 2.0

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 Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr
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Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile	
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Ser Asn Leu Arg Arg Gln Leu Asp Gly Leu Gly Asn Glu Lys Met Lys	
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 Ser Val Thr Thr Val Ser Ser Lys Arg Tyr

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tctgcactga tatgtacagg gaaagtgaga cacatagaaa ccaactgtaac ctacgtagta 1966

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Phe	Arg	Cys	Gly	Leu	Pro	Ile	Thr	Ala	Val	Thr	Val	Asn	Gln	Asn	Leu	85	90	95	
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Asp	Ala	Met	Phe	Glu	Ala	Tyr	Ile	Ser	Asn	Leu	Arg	Arg	Gln	Leu	Asp	165	170	175	
Gly	Leu	Gly	Asn	Glu	Lys	Met	Lys	Leu	Glu	Gly	Glu	Leu	Lys	Asn	Met	180	185	190	
Gln	Gly	Leu	Val	Glu	Asp	Phe	Lys	Asn	Lys	Tyr	Glu	Asp	Glu	Ile	Asn	195	200	205	
Lys	Arg	Ala	Ser	Val	Glu	Asn	Glu	Phe	Val	Leu	Leu	Lys	Lys	Asp	Val	210	215	220	
Asp	Ala	Ala	Tyr	Met	Asn	Lys	Val	Glu	Leu	Glu	Ala	Lys	Val	Asp	Ala	225	230	235	240

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 Arg Glu Leu Gln Ser Gln Ile Lys Asp Thr Ser Val Val Val Glu Met
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 Asp Asn Ser Arg Asn Leu Asp Met Asp Ser Ile Val Ala Glu Val Arg
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 Trp Tyr Lys Gln Lys Phe Glu Glu Met Gln Ser Thr Ala Gly Gln Tyr
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 Gly Asp Asp Leu Arg Ser Thr Lys Ala Glu Ile Ala Glu Leu Asn Arg
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 Lys Leu Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly Gly Ala Gln
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Phe	Lys	Leu	Asn	Tyr	Ser	Val	Asp	Glu	Glu	Tyr	Pro	Asp	Leu	Ser	Lys	
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cac	aac	aac	cac	atg	gcc	aag	gtg	ctg	act	aag	gaa	atg	tat	ggc	aag	208
His	Asn	Asn	His	Met	Ala	Lys	Val	Leu	Thr	Lys	Glu	Met	Tyr	Gly	Lys	
				30					35					40		

ctt	agg	gac	aag	cag	acc	cca	cct	gga	ttc	act	gtg	gat	gat	gtc	atc	256
Leu	Arg	Asp	Lys	Gln	Thr	Pro	Pro	Gly	Phe	Thr	Val	Asp	Asp	Val	Ile	
			45					50					55			

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Gln	Thr	Gly	Val	Asp	Asn	Pro	Gly	His	Pro	Phe	Ile	Met	Thr	Val	Gly	
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tgt	gtt	gct	ggt	gat	gag	gag	tcc	tac	gat	gtt	ttc	aag	gac	ctg	ttc	352
Cys	Val	Ala	Gly	Asp	Glu	Glu	Ser	Tyr	Asp	Val	Phe	Lys	Asp	Leu	Phe	
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gac	ccc	gtc	att	tcc	gac	cgt	cac	ggt	gga	tac	aag	gca	act	gac	aag	400
Asp	Pro	Val	Ile	Ser	Asp	Arg	His	Gly	Gly	Tyr	Lys	Ala	Thr	Asp	Lys	
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cac	aag	acc	gac	ctc	aac	ttt	gag	aac	ctg	aag	ggt	ggt	gat	gac	ctg	448
His	Lys	Thr	Asp	Leu	Asn	Phe	Glu	Asn	Leu	Lys	Gly	Gly	Asp	Asp	Leu	
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Asp	Pro	Asn	Tyr	Phe	Leu	Ser	Ser	Arg	Val	Arg	Thr	Gly	Arg	Ser	Ile	
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Lys	Gly	Tyr	Pro	Leu	Pro	Pro	His	Asn	Ser	Arg	Gly	Glu	Arg	Arg	Ala	
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Val	Glu	Lys	Leu	Ser	Val	Glu	Ala	Leu	Ser	Ser	Leu	Asp	Gly	Glu	Phe	
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Gln	Leu	Ile	Ala	Asp	His	Phe	Leu	Phe	Asp	Lys	Pro	Val	Ser	Pro	Leu	
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cac ctg cgt gtc att tcc atg cag aag ggt ggc aac atg aag gaa gtg			832
His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val			
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Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys			
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Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu			
270	275	280	
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Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val			
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Lys Leu Pro Lys Leu Ser Thr His Ala Lys Phe Glu Glu Ile Leu Thr			
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Arg Leu Arg Leu Gln Lys Arg Gly Thr Gly Gly Val Asp Thr Ala Ser			
315	320	325	
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Val Gly Gly Val Phe Asp Ile Ser Asn Ala Asp Arg Ile Gly Ser Ser			
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gag gtt gag cag gtg cag tgt gtg gtt gat ggt gtc aag ctg atg gtg			1168
Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val			
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gag atg gag aag aag ctg gga gaa ggc cag tcc atc gac agc atg atc			1216
Glu Met Glu Lys Lys Leu Gly Glu Gly Gln Ser Ile Asp Ser Met Ile			
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Pro Ala Gln Lys			
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Val Leu Thr 35	Lys Glu Met Tyr 40	Gly Lys Leu Arg Asp 45	Lys Gln Thr Pro
Pro Gly Phe Thr 50	Val Asp Asp 55	Val Ile Gln Thr Gly 60	Val Asp Asn Pro
Gly His Pro Phe 65	Ile Met Thr 70	Val Gly Cys Val 75	Ala Gly Asp Glu Glu 80
Ser Tyr Asp Val 85	Phe Lys Asp Leu 90	Phe Asp Pro Val 95	Ile Ser Asp Arg
His Gly Gly Tyr 100	Lys Ala Thr Asp 105	Lys His Lys Thr 110	Asp Leu Asn Phe
Glu Asn Leu 115	Lys Gly Gly Asp 120	Asp Leu Asp Pro 125	Asn Tyr Phe Leu Ser
Ser Arg Val Arg 130	Thr Gly Arg Ser 135	Ile Lys Gly Tyr 140	Pro Leu Pro Pro
His Asn Ser Arg 145	Gly Glu Arg Arg 150	Ala Val Glu Lys 155	Leu Ser Val Glu 160
Ala Leu Ser Ser 165	Leu Asp Gly Glu 170	Phe Lys Gly Lys 175	Tyr Tyr Pro Leu
Lys Ser Met Thr 180	Asp Asp Glu Gln 185	Glu Gln Leu Ile 190	Ala Asp His Phe
Leu Phe Asp 195	Lys Pro Val Ser 200	Leu Leu Leu Ala 205	Ala Gly Met Ala
Arg Asp Trp 210	Pro Asp Ala Arg 215	Gly Ile Trp His 220	Asn Glu Asn Lys Ala
Phe Leu Val Trp 225	Val Lys Gln Glu 230	Asp His Leu Arg 235	Val Ile Ser Met 240
Gln Lys Gly Gly 245	Asn Met Lys Glu 250	Val Phe Lys Arg 255	Phe Cys Val Gly
Leu Gln Arg 260	Ile Glu Glu Ile 265	Phe Lys Lys His 270	Asn His Gly Phe Met
Trp Asn Glu 275	His Leu Gly Phe 280	Val Leu Thr Cys 285	Pro Ser Asn Leu Gly
Thr Gly Leu Arg 290	Gly Gly Val 295	His Val Lys Leu 300	Pro Lys Leu Ser Thr
His Ala Lys Phe 305	Glu Glu Ile Leu 310	Thr Arg Leu Arg 315	Leu Gln Lys Arg 320
Gly Thr Gly Gly 325	Val Asp Thr Ala 330	Ser Val Gly Gly 335	Val Phe Asp Ile
Ser Asn Ala Asp 340	Arg Ile Gly Ser 345	Ser Glu Val Glu 350	Gln Val Gln Cys

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 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn
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 Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
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 Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg
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 Leu Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met
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 Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
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 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
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 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
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 Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro
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 gcc cag aac acc ggg ctc ggt cct gag aag acc tct ttc ttc cag gct 494

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Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala
 125 130 135 140

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 Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser
 — 145 150 155

gac gtt cag ctt atc aaa cct gga gac aag gtg ggc gcc agc gag gcc 590
 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
 160 165 170

acg ctg ctg aac atg ctg aac atg ctg aac atc tgc ccc ttc tcc tac 638
 Thr Leu Leu Asn Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr
 175 180 185

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 Gly Leu Ile Ile Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro
 190 195 200

gag gtg ctg gac atc act gag gac gcc ctg cac aag agg ttc ctg aag 734
 Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys
 205 210 215 220

ggt gtg agg aac atc gcc agt gtg tgt ctg cag atc ggc tac cca act 782
 Gly Val Arg Asn Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr
 225 230 235

ctt gct tcc atc cct cac act atc atc aat gga tac aag agg gtc ctg 830
 Leu Ala Ser Ile Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu
 240 245 250

gct gtc act gtc gaa aca gac tac aca ttc ccc ttg gct gag aag gtg 878
 Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val
 255 260 265

aag gcc tac ctg gct gat ccc acc gct ttc gct gtt gca gcc cct gtt 926
 Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val
 270 275 280

gcg gca gct aca gag cag aaa tcc gct gct cct gcg gct aaa gag gag 974
 Ala Ala Ala Thr Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu
 285 290 295 300

gca ccc aag gag gat tct gag gag tct gat gaa gac atg ggc ttc ggc 1022
 Ala Pro Lys Glu Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly
 305 310 315

ctg ttt gat taa accagacacc gaatatccat gtctgttttaa catcaataaa 1074
 Leu Phe Asp 320

acatctggaa acaaaaaaaaaa aaaaaaaaaa 1104

<210> 6
 <211> 319
 <212> PRT
 <213> Danio rerio

<400> 6
 Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys
 1 5 10 15

Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe Ile Val Gly Ala
 20 25 30

- 34 -

Asp Asn Val Gly Ser Lys Gln Met Gln Thr Ile Arg Leu Ser Leu Arg
 35 40 45
 Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
 50 55 60
 Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro
 65 70 75 80
 His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
 85 90 95
 Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
 100 105 110
 Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
 115 120 125
 Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
 130 135 140
 Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
 145 150 155 160
 Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
 165 170 175
 Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
 180 185 190
 Gln Gln Val Tyr Asp Asn Gly Ser Val Tyr Ser Pro Glu Val Leu Asp
 195 200 205
 Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys Gly Val Arg Asn
 210 215 220
 Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
 225 230 235 240
 Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
 245 250 255
 Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
 260 265 270
 Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
 275 280 285
 Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
 290 295 300
 Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
 305 310 315

<210> 7
 <211> 2241
 <212> DNA
 <213> Danio rerio

 <220>
 <221> TATA_signal
 <222> (2103)..(2108)

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<220>
<221> primer_bind
<222> (2221)..(2241)
<223> CK2

<220>
<221> misc_feature
<222> (2142)..(2235)
<223> Identical to the 5' CK cDNA

<400> 7
ccttcccttc tacttttgac gtccttttaa gagcttgtgc atgaaagcag atttggagct 60
gattactcat ctcaaacacc catacaaagg gatgattgcc gtaccatgat ctcacacctt 120
tcacacctgg ttatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180
cagtgtggtc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240
aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggg cattaaatac 300
tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
gtgtgtgaag taacaaatga caaatactca aactattgta attaagtagt ttttctcaga 420
aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttcccttg agtacatttt 480
tagtgcagtg ttggtacttt tatttcactt ccttccctca acctgcagtc actactttat 540
ttattcttgt ctatgtggat tagacaaatc agtcctgtga ttctgttcca atcaaattgc 600
acatagaagg taaatcacat cataatgaac taccttaaga catgggccat ttataattgc 660
agcaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaacccag 720
agactgctta gatgcatgtc actgatgaga agatgatgga tgtttactgt atgatgaccg 780
aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcggtta gggtgacgtt 840
gtaccccaac gcagtgggga cggtgcattt tgtttagaaa tgaaaattag gttgacgtca 900
gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960
ctaagatgt tacagcttga tgttatgagg atgttaccac tatgacgtct atcagacgtt 1020
ggattatggt tgccatacct gatgaataaa tgtcattatt tgacgttggt ttaagatgtt 1080
ggttcgacat tggattttgg tcgctttcca acacaacct aatccaccaa atattaactt 1140
cctatgacat cgttattgga cgtcaaaata acaatatcct tagatgctgg ctagactttg 1200
aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260
tgctgggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320
taaatgcac agcttttcac agcataatac tcactactta ctactcttga gtacttttaa 1380
aaaagctact tttcactcat actttgagta atatttaca ctgatacttt tactcgcaact 1440
acatttttag gcatgtattg atatttttac tatgattttt cagtactctt tccactactg 1500
cagccctccc catacataat cgtatgttta cacatatggt ggagtttaga gccataatct 1560
acattagctt tgttagccgc tagcattact gtgcagaatt gtgtgtgtgc acattttcca 1620

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atatcaatac agaaggaaac tgtgttcctt gttcccttgt aaatctcaac aatgcaactg 1680
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaag tgaatggaaa 1740
 aaagcctttc attaatgtga aagtgtgtgc gcgccccacc cagataaaaa gagcagaggt 1800
 taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgcgtgg 1860
 cagatggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
 ctcaagcctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
 caacatttat ctaccactt tctctctgta cctgtctaac aggtaggggtg tgtgtgagag 2040
 tgcgtatgtg tgcaagtgcg tgtgtgtgtg agagcagtca gctccaccct ctcaagagt 2100
 tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
 tgagcaacct cctccactca ctctctctc agagagcact ctctacctc cttctcagca 2220
 actcaaagac acaggatccg g 2241

<210> 8
 <211> 1456
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA_signal
 <222> (1389)..(1394)

<220>
 <221> primer_bind
 <222> (1433)..(1456)
 <223> MCK2

<220>
 <221> misc_feature
 <222> (1428)..(1453)
 <223> Identical to the 5' MCK cDNA

<400> 8
 gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
 tgtggcttaa tcttggtga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
 gcatgtgcac catgacaggc ctgttattca cacttgggtgc catgttggag actgttcggc 180
 cagctatagt tttcttcaca ggtcctggg tcacctaatg tcacaaggaa gaaacatgtt 240
 acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
 ttacagctta aaagattgct agacagaaaa accaggaggg ggttttccca taatatccag 360
 tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgctc 420
 gtgacagaaa accagagatg gaaatacctt cttttgaatt gcataattgc ttaaaagaag 480
 acacaacagg gatagttcac ccaaaaaaca gaccattctt ttttctgtt gaacaaaaat 540
 taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
 aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaac 660

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acatctcaaa taggtttgag gttgaataaa ctttttcat tttggggtgg actatcccta 720
attatttgac acttaagatt tatagtaaatt ctttttatag actttctccc cttattaaac 780
atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccttg 840
tcaaattgtt ttgtgtatgg ttggcgcaca atagactgaa ctggcctatc acacagactt 900
tcataacaac tccagttgat gccctttcac cctcagtga taaatatggc gtctgacatg 960
agcagattaa acacgacact gcaacaactt tacctgtaaa aatacaaatt gagtttgac 1020
ccagaatcat gtggtgaacg aagcctacca agagattttt gaaagccatc ggctgacac 1080
gcgcacttct gatattctgtg gtatgtttgg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccatc accctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaatgg atatgggaag gaaggggggc accaccaca gctgccacct 1260
catctaggat gcctggggcc taaattgaag cttttcttac actaaacagg gcataagaga 1320
ccagcgccag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcaggg 1380
gctagaggta tatatatoca aatcaaaactc ttcttgcttg ggtgacctt atttcggctt 1440
ggtgaacagg atccgg 1456

<210> 9
<211> 2205
<212> DNA
<213> Danio rerio

<220>
<221> primer_bind
<222> (2179)..(2205)
<223> ARP2

<220>
<221> misc_feature
<222> (2153)..(2199)
<223> Identical to the 5' ARP cDNA

<220>
<221> intron
<222> (792)..(2152)

<220>
<221> misc_feature
<222> (775)..(791)
<223> Identical to the 5' ARP cDNA

<400> 9
atctgtatta agaaacactt aaaatatata tgcgttacga attaaaaaca aaacacgatc 60
attttaattt gtgttgata attttacatt ttgtaagtat tatttttata aaaaatatat 120
agaaataata caaatttgtt tacagtattc ttagttattg caataaacga attttatata 180
gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggtc aattcattaa 360

aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
gtgcagattt ttggtgttg ttagaagga tacatctgcg gccgaaagt aacgggaact 480
attt-acattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatgc 600
tatattgacc gcagctgtat ccttttctaag tgcgactgta caaatacgca ctgaccgtga 660
cagacacgtg cattgaccaa tcagcgcaca gatacgcatt ttccgcgcga ttctgattgg 720
atgatcgact gatactaata ttgtgccgct tcctttcgcg gcctctttct ttcacgcgtc 780
cctaccgtga ggtaaggctg acgcgcgtct. tgtggcggtt tcttaaaatg tgtaataaaa 840
taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
tatgcgttta aagcttgtgt aatgattttt acagtaaaaag ttagcactag cctgttagca 960
caggcctcgt gcgccatgtg tgacgcgacg ttttaatagc atcttatttg attttgatga 1020
tccgattctg atattaatca tatttatgcg taaaatgtgt gatgggtctg ctagtggaca 1080
ttacatgcta gtacttgtgc tagtcggtcg atccacattg agatgttgcg ctatttgcca 1140
ttttaaaacc agttactctc atttttagtga aatattctta agccactaag ttaaaatttg 1200
tcaatcacat ataattgtgt ttatgtttta ttgagtcac cataccaggt aatagtttta 1260
tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
gtaaagttaa tcttaagggt gtaaaggctc acccaaaaga caattcacgc tcaagtgttt 1380
tcaaacttta tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
accataatac aaatacagga aaaatatact atagaagtcg atggttacag gttttctgca 1500
ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
tgcataaatc agttttcatt tgggtgagct gtctctaaac atttgattta gacacctcag 1620
gcagtggcca ccaagcttgt tcctgaaggg ccagtgtcct acagatttta gctccaaccc 1680
taattaaaca cacctgaaca agctaataca ggtcttacta ggtatgtttg aaacatccag 1740
gcaggtgtgt tgatgcaaga tagagctaaa ccctgcaggg acaatggccc aacaggattg 1800
gtgacccctg cctcaagcca tcacaaatgc attatggtat taagaaatgt gcaggttcag 1860
ttatggacag gctgttgag tgcttgttcg tcgttccac tgcacaaatg aacatgattc 1920
cttctatccc tgtctgtctg catctcatga cttgcaggga cgctgggtctc agacacgttt 1980
atagcagtaa atcaaataca atagtgtctt gattatcttt aaatatttga aagcttataa 2040
taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaaat 2100
aagatgcaca caaggcaggt gtaaaagtat tgcttgtgtt tgtaatcctc agattttaca 2160
accttgtctt taaaccggct gttcaccgat ccttgaagg gatcc 2205

<210> 10

<211> 24

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
— gene specific primer

<400> 10
cgctggagta agagatagac ctgg

24

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cytokeratin
gene specific primer

<220>
<221> misc_feature
<222> (1)..(6)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 11
ccggatcctg tgtctttgag ttgctg

26

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 12
ccggatcctt gggatcagat cctg

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc_feature

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<222> (3)..(8)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa

24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc

25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca

26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<400> 16
gttcattctt acaagctagc gctgaacaat gctgtggaca agcttgaatt c

51

<210> 17
<211> 10

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

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<220>

<223> n is a dideoxycytidine

<400> 17

gaattcaagn

10

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 18

gttcattcttt acaagctagc g

21

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: linker
specific primer

<400> 19

tcctgaacaa tgctgtggac

20

<210> 20

<211> 1392

<212> DNA

<213> Danio rerio

<220>

<221> CDS

<222> (42)..(551)

<220>

<221> primer_bind

<222> (6)..(28)

<223> M2

<220>

<221> primer_bind

<222> (23)..(45)

<223> M1

<220>

<221> polyA_signal

<222> (797)..(802)

<220>

<221> polyA_signal

<222> (1351)..(1357)

<400> 20

ctcttcttga tcttcttaga cttcacacat accgtctcga c atg gca ccc aag aag 56

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Met Ala Pro Lys Lys
1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
 Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
 — 10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
 Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
 25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
 Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
 40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
 Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
 55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
 Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
 70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
 Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
 90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
 Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
 105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
 Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
 120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
 Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
 135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
 Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
 150 155 160 165

gag aag gag gag taa acaaccttgg aatcaagaaa acgaagagaa gaacatgcat 591
 Glu Lys Glu Glu
 170

cctcacagct taatctccag tctgttctct ggcttctct aacttttgtt tttccttct 651
 ccctttcttg ctttctacca tctgtgttac tccaagcact tacactctcc atcttaccaa 711
 agacttctct cgctgggact gaattgggag ggtggagagg aacacgacca cagtgtctgt 771
 cgagtgggga catgggattg ttttcaataa aatgaacatc atttctgtat ctctcacatt 831
 ctctctttct ctctgtttct cactcattac ccacaacccc tctctttcat ttcagtcaag 891
 cttgcatgta agtcgctgct tcttctgctg cagtcttagg agttgaaacg aaggcatcta 951
 tagtttgggg ctgaaacatc tctctagatc aatgtggaag agtgctcact ctgaggggga 1011
 aagaagcacg atggagtgat ctactctat aatagaggaa ccagtcatca ttctcatttc 1071

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ctcctctggt ggttgactaa aaagagaaa agaaaatgag ggttttgtgc tgagtgagtt 1131
tagcctccta aaagcgatgc cgagctcatc acagagggag tgagagggac agaccatcct 1191
aggaagagag gagagcaggg actgaaagaa aacataacct cttcactccc cctctcccct 1251
cctctctctc atttctctgt ccctcttttc tttttctttt tttctttttt gctttctgca 1311
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aataaaaaaa aaaaaaaaaa a 1392

<210> 21
<211> 169
<212> PRT
<213> Danio rerio

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1 5 10 15
Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
20 25 30
Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
35 40 45
Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
50 55 60
Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65 70 75 80
Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
85 90 95
Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
100 105 110
Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
115 120 125
Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
130 135 140
Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145 150 155 160
Ile Thr His Gly Glu Glu Lys Glu Glu
165

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)

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<223> E-box, canntg

<220>
<221> enhancer
<222> (452)..(457)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1095)..(1100)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1278)..(1283)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1362)..(1367)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1385)..(1390)
<223> E-box, canntg

<220>
<221> enhancer
<222> (523)..(532)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (606)..(615)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (697)..(706)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1490)..(1499)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1640)..(1649)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<221> enhancer
<222> (1956)..(1965)
<223> Potential MEF2 binding site, yta(w)4tar

<220>
<223> Transcription start site at residue 2012

<220>
<221> primer_bind
<222> (2032)..(2054)
<223> M2

<220>
<221> misc_difference
<222> (2027)..(2054)
<223> Identical to the 5' MLC2f cDNA

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- 46 -

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<223> Description of Artificial Sequence: MLC2F gene
specific primer M1

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<220>
<223> Description of Artificial Sequence: MLC2F gene
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